

gi|7661964|ref|NP_055552.1| MDYSHQTSLVPCGQDKYISKNEILLHLKTYNLYYEGONLQLRHREEEDEFIVEGLLNISWGLRRPRLQMODDNERIRPPSSSSWHS GCN LGAGTTLKPLTVPKVQISEVDAPPEGDMPSTDSRG-LKPLQEDTPOLMRTRSDVGV 150
gi|114680788|ref|XP_514496.2| MDYSHQTSLVPCGQDKYISKNEILLHLKTYNLYYEGONLQLRHREEEDEFIVEGLLNISWGLRRPRLQMODDNERIRPPSSSSWHS GCN LGAGTTLKPLTVPKVQISEVDAPPEGDMPSTDSRG-LKPLQEDTPOLMRTRSDVGV 150
gi|73991749|ref|XP_542904.2| MDYSHQTSLVPCGQDKYISKNEILLHLKTYNLYYEGONLQLRHREEEDEFIVEGLLNISWGLRRPRLQMODDNERIRPPSSSSWHS GCN LGAGTTLKPLTMPNIQISEVDAPPEGDTSSPTDSRG-LKPLQEDTPOLMRTRSDVGV 150
gi|30425302|ref|NP_780654.1| MDYTHQPALIPCQDKYMPKSELLHLKTYNLYYEGONLQLRHREEEDEFIVEGLLNISWGLRRPRLQMODDNERIRPPSSSSWHS GCN LGAGTTLKPLTMPNIQISEVDMPVGLTHSPDSRG-LKPVQEDTPOLMRTRSDVGV 150
gi|79749367|ref|NP_001032173.1| MDYTHQPALIPCQDKYMPKSELLHLKTYNLYYEGONLQLRHREEEDEFIVEGLLNISWGLRRPRLQMODDNERIRPPSSSSWHS GCN LGAGTTLKPLTVPTVQISEVDMPVNMMEHSPDSRG-LKPVQEDTPOLMRTRSDVGV 150
gi|71894699|ref|NP_001026055.1| MEYGSCEYLVPCGQDKYISKNEILLHLKTYNLYYEGONLQLRHREEEDEFIVEGLLNISWGLRRPRLQMODDNERIRPPSSSSWHS GCN LGAGTTLKPLTVPTVQISEVDMPVNMMEHSPDSRG-LKPVQEDTPOLMRTRSDVGV 150
gi|52219184|ref|NP_001004676.1| MDDRIDG--VRVRENKFKISKSSILLHLKTYNLYYEGONLQLRHREEEELIMEGLLNISWGLRRPRLQMODDNERIRPPSSSSWHS GCN LGAGTTLKPLTVPTVQISEVDMPVNMMEHSPDSRG-LKPVQEDTPOLMRTRSDVGV 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150



gi|7661964|ref|NP_055552.1| RRRGNVRTPSDQRRIRRRHRSINGHFYNHKTAVFTPAYGSVTNVRINSTMTTPQVLRVLLNKFKFIENSPPDFALYLVHSGERVQLKRTDYPLVVRILQGPCHEVCRIFLMEODLGEIIFVEVAQYIKFEMPVLSFTIKLKEEDREVE 300
gi|114680788|ref|XP_514496.2| RRRGNVRTPSDQRRIRRRHRSINGHFYNHKTAVFTPAYGSVTNVRINSTMTTPQVLRVLLNKFKFIENSPPDFALYLVHSGERVQLKRTDYPLVVRILQGPCHEVCRIFLMEODLGEIIFVEVAQYIKFEMPVLSFTIKLKEEDREVE 300
gi|73991749|ref|XP_542904.2| RRRGNVRTPSDQRRIRRRHRSINGHFYNHKTAVFTPAYGSVTNVRINSTMTTPQVLRVLLNKFKFIENSPPDFALYLVHSGERVQLKRTDYPLVVRILQGPCHEVCRIFLMEODLGEIIFVEVAQYIKFEMPVLSFTIKLKEEDREVE 300
gi|30425302|ref|NP_780654.1| RRRGNVRTPSDQRRIRRRHRSINGHFYNHKTAVFTPAYGSVTNVRINSTMTTPQVLRVLLNKFKFIENSPPDFALYLVHSGERVQLKRTDYPLVVRILQGPCHEVCRIFLMEODLGEIIFVEVAQYIKFEMPVLSFTIKLKEEDREVE 300
gi|79749367|ref|NP_001032173.1| RRRGNVRTPSDQRRIRRRHRSINGHFYNHKTAVFTPAYGSVTNVRINSTMTTPQVLRVLLNKFKFIENSPPDFALYLVHSGERVQLKRTDYPLVVRILQGPCHEVCRIFLMEODLGEIIFVEVAQYIKFEMPVLSFTIKLKEEDREVE 300
gi|71894699|ref|NP_001026055.1| RRRGSSRTPSEQRRIRRRHRSINGHFYNHKTAVFTPAYGSVTNVRINSTMTTPQVLRVLLNKFKFIENSPPDFALYLVHSGERVQLKRTDYPLVVRILQGPCHEVCRIFLMEODLGEIIFVEVAQYIKFEMPVLSFTIKLKEEDREVE 300
gi|52219184|ref|NP_001004676.1| LRRGRRSVPSDQRRIRRRHRSINGHFYNHKTAVFTPAYGSVTNVRINSTMTTPQVLRVLLNKFKFIENSPPDFALYLVHSGERVQLKRTDYPLVVRILQGPCHEVCRIFLMEODLGEIIFVEVAQYIKFEMPVLSFTIKLKEEDREVE 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300



gi|7661964|ref|NP_055552.1| KLMRKYTTLRLMIRQRLLEEIAETPATI 327
gi|114680788|ref|XP_514496.2| KLMRKYTTLRLMIRQRLLEEIAETPATI 327
gi|73991749|ref|XP_542904.2| KLMRKYTTLRLMIRQRLLEEIAETPATI 327
gi|30425302|ref|NP_780654.1| KLMRKYTTLRLMIRQRLLEEIAETPETI 327
gi|79749367|ref|NP_001032173.1| KLMOKYTTLRLMIRQRLLEEIAETPETI 327
gi|71894699|ref|NP_001026055.1| KLMRKYSILLRMIEQRLLEEISEGPARL 327
gi|52219184|ref|NP_001004676.1| KLKSRVYKCLRCIEKQLCLPEGSTCM 327
.....310.....320.....

